

#6



#6

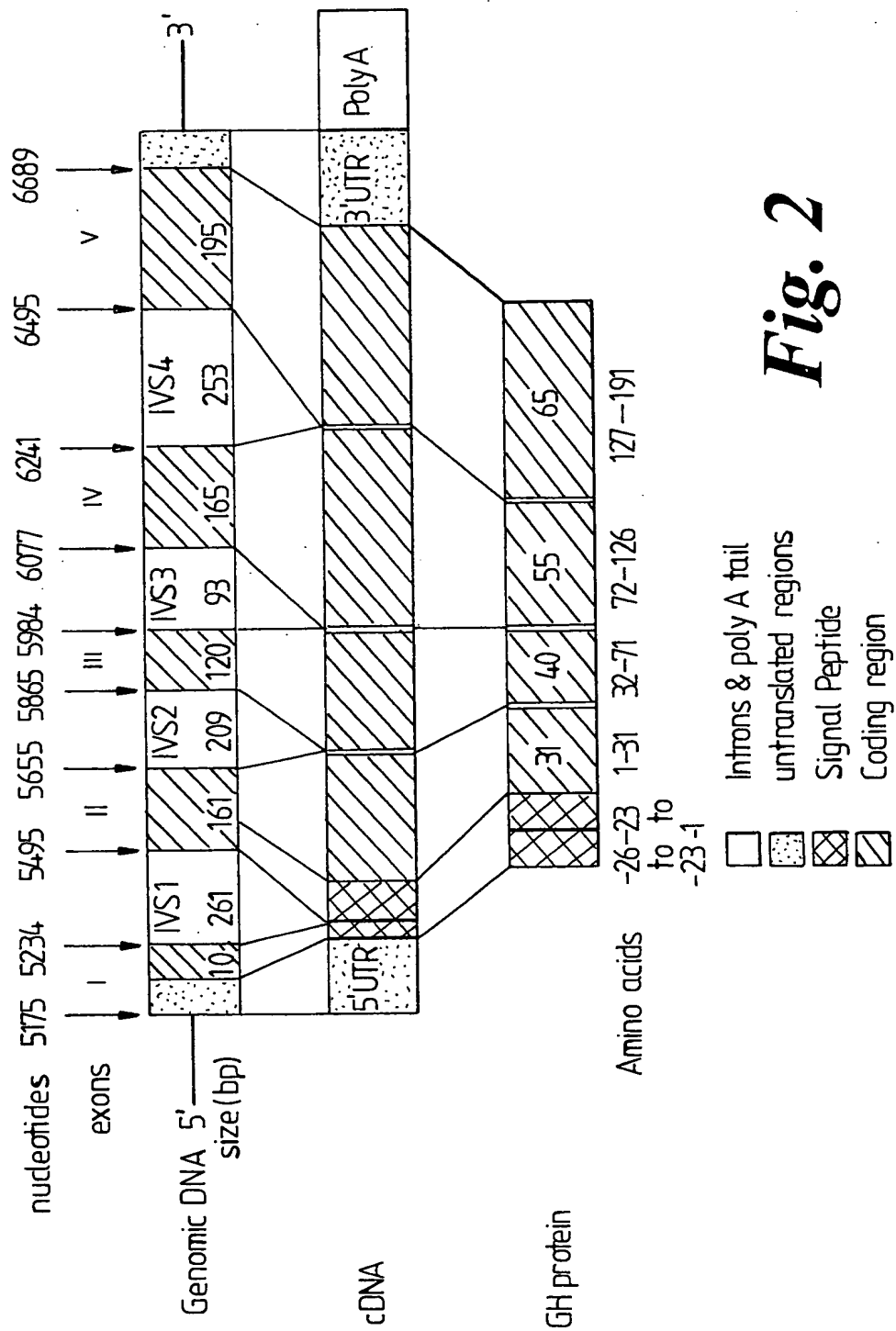


Fig. 2

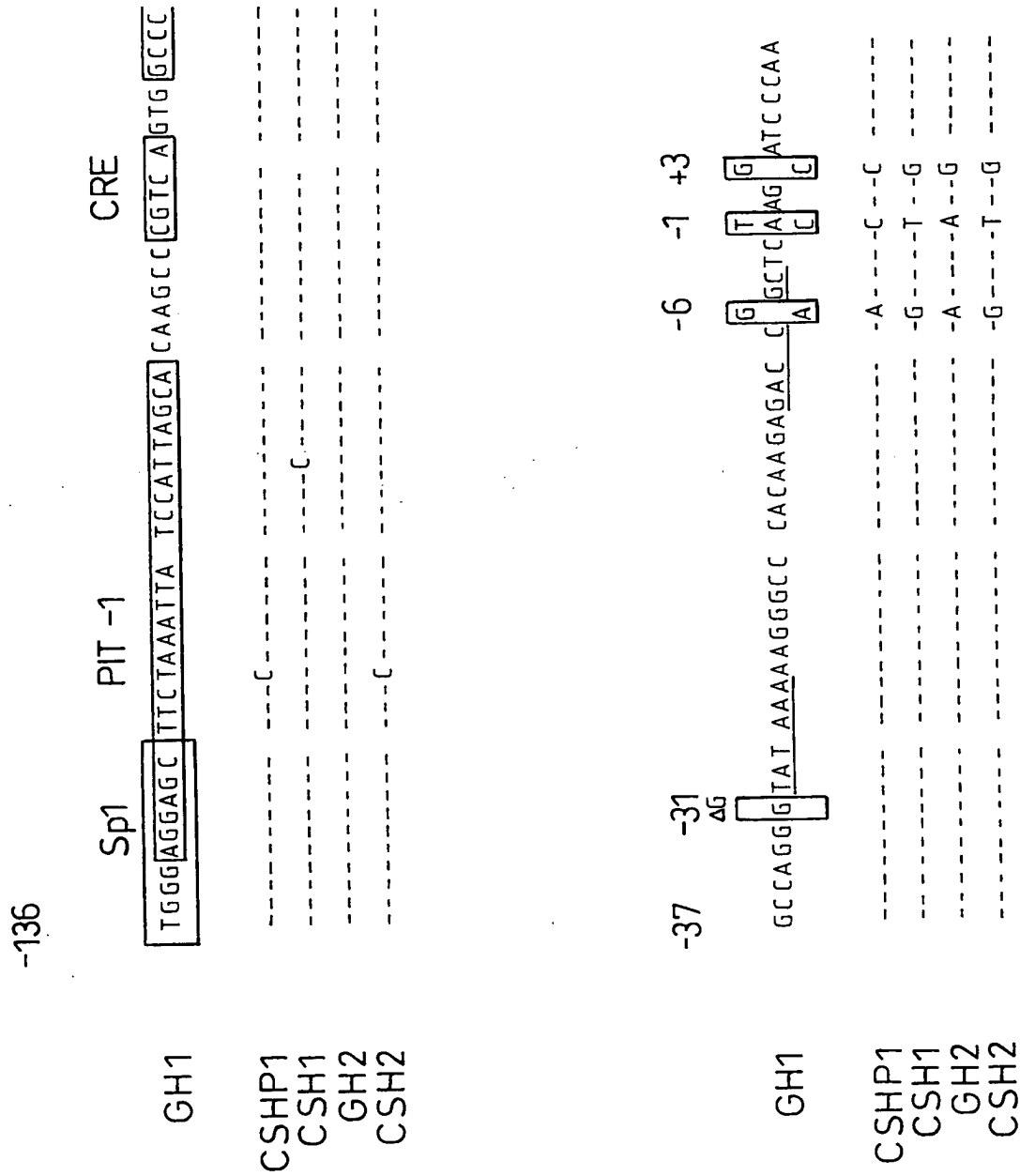


Fig. 3

Figure 4

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tccgaggaaacagccccgttccgggcagccccagatgttcttctgtttccagatgttccaaatgaaaaaacattt 151-225
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301-375
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GenBank

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 tgtaactccggtaggacgtagactccatgaaccacttacaccacctgccgtgcgggactcctcccgtcctcac
 cgagg 2026-2030
 gctcc
 25 PCR primers are marked in bold (42-1984 = 1942bp).
 Sequencing primers are underlined (GHLCR3.1, 541-558; GHLCR3.2, 1006-1023; GHLCR3.3, 1422-1440;
 GHLCR5.0, 640-658)

Figure 5

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	-600	gctcaggga	aggggagagc	aaagtgtggg	gttggttctc	tctagtgggc	-551
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	-500	agaagtggaa	ttcaggactg	aatcgtgctc	acaacccccca	caatctattg	-451
	-450	gctgtgcttg	gccccctttc	ccaacacaca	cattctgtct	ggtgggtgga	-401
10	-400	ggttaaacat	gcggggagga	ggaaagggat	aggatagaga	atgggatgtg	-351
	-350	gtcggtaggg	ggtctcaagg	actggctatc	ctgacatcct	tctccgcgtt	-301
	-300	caggttggcc	accatggcct	gcgggccagag	ggcaccacag	tgacccttaa	-251
	-250	agagaggaca	agttgggtgg	tatctctggc	tgacactctg	tgacacaacc	-201
	-200	tcacaacact	ggtgacgggt	ggaaggga	gatgacaagc	cagggggcat	-151
15	-150	gatcccagca	tgtgtgggag	gagcttctaa	attatccatt	agcacaagcc	-101
	-100	cgtcagtggc	cccatgcata	aatgtacaca	gaaacagggtg	gggggagacag	-51
	-50	tgggagagaa	ggggccagggt	tataaaaagg	gcccacaaga	gaccagctca	-1
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	+51	cacctagcgg	caATGGCTAC	AGgttaagcgc	ccctaaaatc	cctttgggca	+100
20	+101	caatgtgtcc	tgaggggaga	ggcagcgacc	tgtagatggg	acggggggcac	+150
	+151	taaccctcag	gtttggggct	tctgaatgtg	agtatcgcca	tgtaagccca	+200
	+201	gtatttgcc	aatctcagaa	agctcctgg	ccctggagg	atggagagag	+250
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	+401	TTCCCAACCA	TTCCCTTATC	CAGGCTTTT	GACAACGCTA	TGCTCCGCGC	+450
	+451	CCATCGTCTG	CACCAGCTGG	CCTTTGACAC	CTACCAGGAG	TTTgtaagct	+500
	+501	cttggggaat	gggtgcgcac	cagggtggc	aggaagggt	gactttcccc	+550
	+551	gcgtgggaaa	taagaggag	agactaagg	gctcagggt	tttcccgag	+600
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	+1201	cttcatttcc	cctcgtgaat	cctccaggcc	tttctctaca	ccctgaagg	+1250
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	+1751	agctggagtg	cagtggcaca	atcttggtc	actgcaatct	ccgcctcctg	+1800
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Figure 5 (continued)

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	+2351	cttttgctta	tctagatatg	cccatctgcc	tggtacaatc	tctggcacat	+2400
	+2401	gttacaggca	acaactactt	gtggaattgg	tgaatgcatg	aatagaagaa	+2450
	+2451	tgagtgaatg	aatgaataga	caaaaggcag	aaatccagcc	tcaaagaact	+2500
	+2501	tacagtctgg	taagaggaat	aaaatgctcg	caaatcgcca	caggcacggt	+2550
10	+2551	caaaggaagg	aggggctatt	tccagctgag	ggcaccgccat	caggaaagca	+2600
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	+2651	tatcaatgga	tctgtctccat	ggagaataat	ccccaaagtg	aaattactta	+2700
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	+2751	atcaaccagt	gcaaacaaatc	cccccatcaa	tacacagcag	tgcttgcctc	+2800
15	+2801	tctccccccg	aggtcttccg	aggcccttcc	tccgtgcctg	aacccctctg	+2850
	+2851	acatatcata	tggcaaatcg	aagtgtccaa	cgagatatag	gaagtgaac	+2900
	+2901	acgatgtaca	ctgaaacgtg	caatacaaat	atgcagcatg	aagtgcctcg	+2950
	+2951	gttactaatac	cagagctacg	ctgggtgctt	cttttctacc	actttcctta	+3000

20

THE **NEW** **YORK** **PUBLIC** **LIBRARY**

Figure 6

Growth hormone 1
 5 Gene symbol : *GHI*
 Location : 17q

1 2

10 -26 ATG GCT ACA G↓GC TCC CGG ACG TCC CTG CTC CTG GCT TTT GGC CTG -12
 Met Ala Thr G ly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu

11 CTC TGC CTG CCC TGG CTT CAA GAG GGC AGT GCC TTC CCA ACC ATT 4
 Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile

15 5 CCC TTA TCC AGG CTT TTT GAC AAC GCT AGT CTC CGC GCC CAT CGT 19
 Pro Leu Ser Arg Leu Phe Asp Asn Ala Ser Leu Arg Ala His Arg

20 CTG CAC CAG CTG GCC TTT GAC ACC TAC CAG GAG TTT↓GAA GAA GCC 34
 Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala

20 35 TAT ATC CCA AAG GAA CAG AAG TAT TCA TTC CTG CAG AAC CCC CAG 49
 Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln

50 ACC TCC CTC TGT TTC TCA GAG TCT ATT CCG ACA CCC TCC AAC AGG 64
 Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg

25 65 GAG GAA ACA CAA CAG AAA TCC↓AAC CTA GAG CTG CTC CGC ATC TCC 79
 Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser

80 CTG CTG CTC ATC CAG TCG TGG CTG GAG CCC GTG CAG TTC CTC AGG 94
 Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg

95 AGT GTC TTC GCC AAC AGC CTG GTG TAC GGC GCC TCT GAC AGC AAC 109
 Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn

35 110 GTC TAT GAC CTC CTA AAG GAC CTA GAG GAA GGC ATC CAA ACG CTG 124
 Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu

125 ATG GGG↓AGG CTG GAA GAT GGC AGC CCC CGG ACT GGG CAG ATC TTC 139
 Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe

40 140 AAG CAG ACC TAC AGC AAG TTC GAC ACA AAC TCA CAC AAC GAT GAC 154
 Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp

45 155 GCA CTA CTC AAG AAC TAC GGG CTG CTC TAC TGC TTC AGG AAG GAC 169
 Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp

170 ATG GAC AAG GTC GAG ACA TTC CTG CGC ATC GTG CAG TGC CGC TCT 184
 Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser

50 185 GTG GAG GGC AGC TGT GGC TTC TAG
 Val Glu Gly Ser Cys Gly Phe *

5 Location : 17q

		1 2		
-26	ATG GCT ACA G↓GC TCC CGG ACG TCC CTG CTC CTG GCT TTT GGC CTG			-12
	Met Ala Thr G ly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu			
10	-11 CTC TGC CTG CCC TGG CTT CAA GAG GGC AGT GCC TTC CCA ACC ATT			4
	Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile			
	5 CCC TTA TCC AGG CTT TTT GAC AAC GCT AGT CTC CGC GCC CAT CGT			19
	Pro Leu Ser Arg Leu Phe Asp Asn Ala Ser Leu Arg Ala His Arg			
15	20 CTG CAC CAG CTG GCC TTT GAC ACC TAC CAG GAG TTT ↓ GGG GAA GCC	2 3		34
	Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Gly Glu Ala			
20	35 TAT ATC CCA AAG GAA CAG AAG TAT TCA TTC CTG CAG AAC CCC CAG			49
	Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln			
	50 ACC TCC CTC TGT TTC TCA GAG TCT ATT CCG ACA CCC TCC AAC AGG			64
	Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg			
25	65 GAG GAA ACA CAA CAG AAA TCC ↓ AAC CTA GAG CTG CTC CGC ATC TCC	3 4		79
	Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser			
	80 CTG CTG CTC ATC CAG TCG TGG CTG GAG CCC GTG CAG TTC CTC AGG			94
	Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg			
30	95 AGT GTC TTC GCC AAC AGC CTG GTG TAC GGC GCC TCT GAC AGC AAC			109
	Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn			
35	110 GTC TAT GAC CTC CTA AAG GAC CTA GAG GAA GGC ATC CAA ACG CTG			124
	Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu			
	125 ATG GGG ↓ AGG CTG GAA GAT GGC AGC CCC CGG ACT GGG CAG ATC TTC	4 5		139
	Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe			
40	140 AAG CAG ACC TAC AGC AAG TTC GAC ACA AAC TCA CAC AAC GAT GAC			154
	Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp			
	155 GCA CTA CTC AAG AAC TAC GGG CTG CTC TAC TGC TTC AGG AAG GAC			169
	Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp			
45	170 ATG GAC AAG GTC GAG ACA TTC CTG CGC ATC GTG CAG TGC CGC TCT			184
	Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser			
50	185 GTG GAG GGC AGC TGT GGC TTC TAG			
	Val Glu Gly Ser Cys Gly Phe *			

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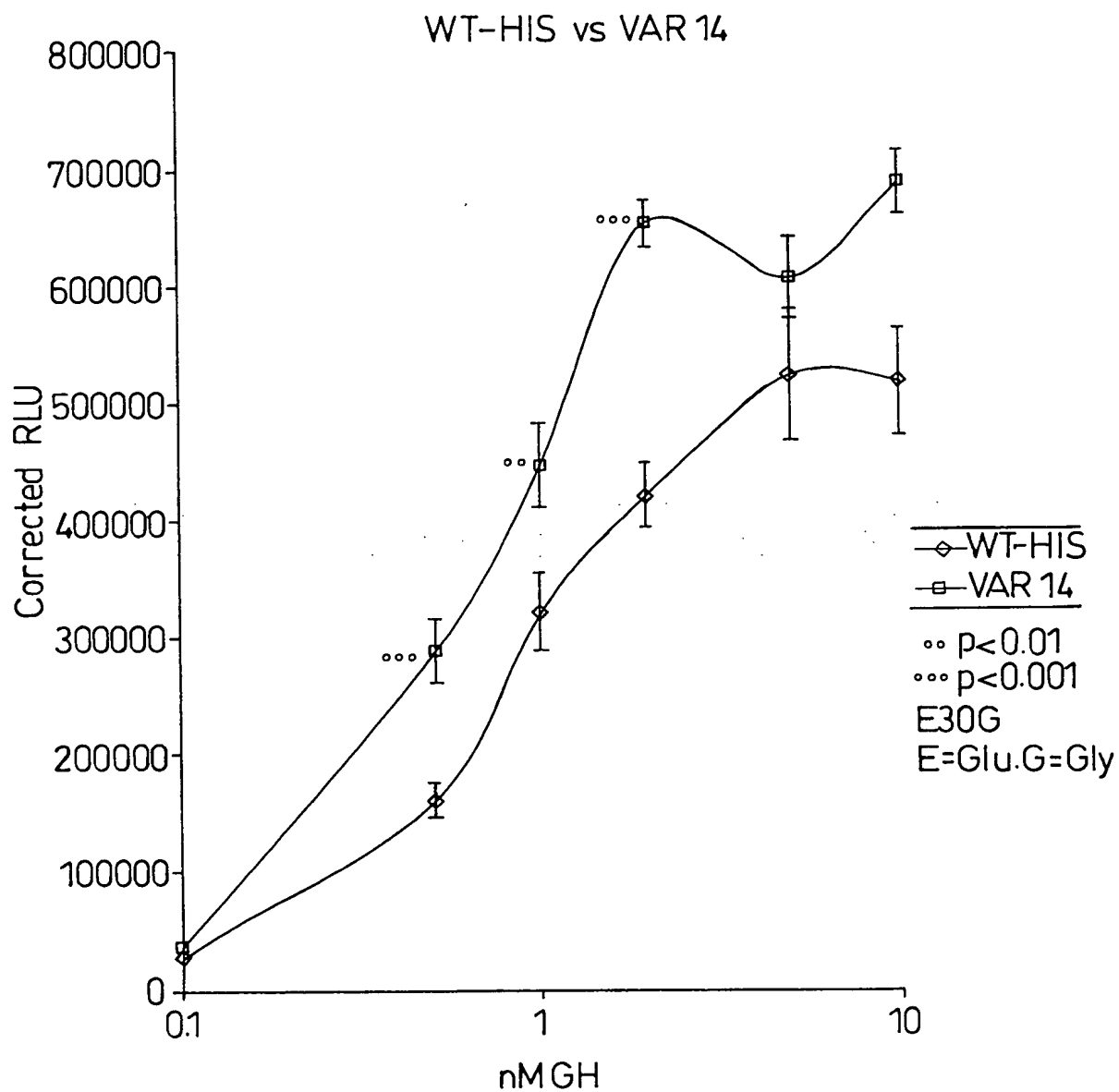


Fig. 8